

IN THE CLAIMS:

Please cancel Claims 5-7, 10-13, and 17-28

Claim 1 (Currently Amended) A method for the expression of a coding region of interest in a *Bacillus sp* comprising:

- a) providing a transformed *Bacillus sp* cell having a chimeric gene comprising a nucleic acid fragment comprising the promoter region of a *Bacillus* gene operably linked to a coding region of interest expressible in a *Bacillus sp*, wherein the nucleic acid fragment comprising the promoter region of a *Bacillus* gene is ~~selected from the group consisting of *narGHJ*, *esn*, *yncM*, *yvyD*, *yvaWXY*, *ydjL*, *sunA*, and *yolHJK*~~ and homologues thereof; and
- b) growing the transformed *Bacillus sp* cell of step (a) in the absence of oxygen wherein the chimeric gene of step (a) is expressed.

Claim 2 (Currently Amended). A method for the expression of a coding region of interest in a *Bacillus sp* comprising:

- a) providing a transformed *Bacillus sp* cell having a chimeric gene comprising a nucleic acid fragment comprising the promoter region of a *Bacillus* gene operably linked to a coding region of interest expressible in a *Bacillus sp*, wherein the nucleic acid fragment comprising the promoter region of a *Bacillus* gene is ~~selected from the group consisting of *narGHJ*, *esn*, *yncM*, *yvyD*, *yvaWXY*, *ydjL*, *sunA*, and *yolHJK*~~ and homologues thereof;
- b) growing the transformed *Bacillus sp.* cell of step (a) in the presence of oxygen whereby the cell density is increased; and
- c) removing oxygen from the transformed *Bacillus sp.* cell or step (b) whereby the chimeric gene is expressed.

Claim 3 (Original) A method according to Claim 2 wherein after step (c) oxygen is re-supplied to the transformed *Bacillus sp.* cell.

Claim 4 (Currently Amended) A method according to either of Claims 1 or 2 wherein ~~the nucleic acid fragment comprising the promoter region of a *Bacillus* gene is contained in a nucleic acid fragment as set forth in~~ selected from the group consisting of SEQ ID NOs:84-15.

Claims 5-7 (Canceled) .

Claim 8 (Currently Amended) A method for the expression of a coding region of interest in a *Bacillus sp* comprising:

- a) providing a transformed *Bacillus sp* cell having a chimeric gene comprising a nucleic acid fragment comprising the promoter region of a *Bacillus* gene operably linked to a coding region of interest expressible in a *Bacillus sp*, wherein the nucleic acid fragment comprising the promoter region of a *Bacillus* gene is ~~selected from the group consisting of yegMN, dhaS rapF, rapG, rapH, rapK, yqhII, yveKLMNOPQST, yhfRSTUV, esn, yneM, yvyD, yvaWXY, ydjL, sunA, and yoliJK, and~~ homologues thereof; and
- b) growing the transformed *Bacillus sp* cell of step (a) in the presence of oxygen until the cell reaches about T0 of the stationary phase wherein the chimeric gene of step (a) is expressed.

Claim 9 (Currently Amended) A method according to Claim 8 wherein the ~~nucleic acid fragment comprising the promoter region of a *Bacillus* gene is~~ contained in a nucleic acid fragment as set forth in ~~selected from the group consisting of SEQ ID NOs: 875, 76, 25-49, and 5-15.~~

Claims 10-13 (Canceled)

Claim 14 (Original) A method according to any of Claims 1, 2 or 3 wherein the expression of the chimeric gene is down-regulated at T0 of the stationary phase.

Claim 15 (Currently Amended). A method according to any one of Claims 1, 2, 3, 4, and 8, ~~10 and 12~~ wherein the *Bacillus sp.* cell is selected from the species consisting of *Bacillus subtilus*, *Bacillus thuringiensis*, *Bacillus anthracis*, *Bacillus cereus*, *Bacillus brevis*, *Bacillus megaterium*, *Bacillus intermedius*, *Bacillus thermoamyloliquefaciens*, *Bacillus amyloliquefaciens*, *Bacillus circulans*, *Bacillus licheniformis*, *Bacillus macerans*, *Bacillus sphaericus*, *Bacillus stearothermophilus*, *Bacillus laterosporus*, *Bacillus acidocaldarius*, *Bacillus pumilus*, and *Bacillus pseudofirmus*.

Claim 16 (Currently Amended) ~~The~~ A method according to any one of Claims 1, 2, 3, 4, and 8, ~~10 and 12~~, wherein the coding region of interest is selected from the group consisting of *crtE crtB, pds, crtD, crtL, crtZ, crtX crtO, phaC, phaE, efe, pdc, adh*, genes encoding limonene synthase, pinene synthase, bornyl synthase, phellandrene synthase, cineole synthase, sabinene synthase, and taxadiene synthase.

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Claims 17-28 (Canceled)
